AMENDMENTS TO THE CLAIMS

1. – 39. (Canceled)

40. (Withdrawn; Currently Amended) A method of making a polypeptide comprising expressing the sequence corresponding to the open reading frame of a polynucleotide according to ~~Claim 38~~ Claim 57.

41. (Currently Amended) A diagnostic reagent for the differential detection of a human endogenous retroviral sequence comprising a polynucleotide having a sequence ~~is~~ selected from the group consisting of SEQ ID NO: ~~1-22, 28, 37-57, 59-61 and 121-122~~ 1, 2, 3-8, 10, 13, 16, 17, 20, 21, and 22, a sequence complementary to one of SEQ ID NO: ~~1-22, 28, 37-57, 59-61 and 121-122~~ 1, 2, 3-8, 10, 13, 16, 17, 20, 21, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: ~~1-22, 28, 37-57, 59-61 and 121-122~~ 1, 2, 3-8, 10, 13, 16, 17, 20, 21, and 22.

42. (Previously Presented) The diagnostic reagent according to Claim 41, wherein said polynucleotide further comprises a label for detection.

43. (Previously Presented) The diagnostic reagent according to Claim 41, wherein said polynucleotide is selected from the group consisting of nucleotides 3065-4390 of SEQ ID NO: 3, nucleotides 6965-9550 of SEQ ID NO: 3, and nucleotides 2502-2865 of SEQ ID NO: 3.

44. – 45. (Canceled)

46. (Withdrawn; Currently Amended) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) contacting a biological sample with at least one diagnostic reagent comprising one or more polynucleotides according to ~~Claim 41~~ Claim 57, and

(b) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction.

47. (Withdrawn; Currently Amended) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) preparing a biological tissue or fluid,

(b) extracting a nucleic acid to be detected,

(c) contacting the nucleic acid with at least one diagnostic reagent comprising one or more polynucleotides according to ~~Claim 41~~ Claim 57,

(d) ~~conducting at least one gene amplification cycle with the aid of said at least one diagnostic reagent,~~

~~(e)~~ detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction, and

~~(f)~~ (e) comparing the nucleic sequences obtained from said detecting with a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1 or at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2, wherein said sequence is selected from the group consisting of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, a sequence complementary to one of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22.

48. (Withdrawn) The method according to Claim 47, wherein said comparing is by a technique selected from the group consisting of sequencing, Southern blotting, restriction cleavage, and SSCP.

49. (Withdrawn; Currently Amended) A method of detecting a polypeptide encoded by a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1 or at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2, wherein said sequence is selected from the group consisting of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, a sequence complementary to one of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, comprising:

collecting messenger RNAs obtained from a control biological sample and from a sample collected from patient, and

analyzing qualitatively and/or quantitatively said mRNAs using ~~the~~ a diagnostic ~~aid~~ reagent comprising one or more polynucleotides according to ~~Claim 41~~ Claim 57 by a technique selected from the group consisting of *in situ* hybridization, by dot-blot, Northern blotting, RNAse mapping and RT-PCR.

50. (Withdrawn; Currently Amended) A recombinant cloning or expression vector comprising the polynucleotide according to ~~Claim 38~~ Claim 57.

51. (Withdrawn; Currently Amended) A method of making a diagnostic reagent comprising mixing the polynucleotide according to ~~Claim 38~~ Claim 57 with a suitable medium.

52. (Withdrawn; Currently Amended) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) making a diagnostic reagent comprising mixing the polynucleotide according to ~~Claim 38~~ Claim 57 with a suitable medium,

(b) contacting a biological sample with said diagnostic reagent, and

(c) detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction.

53. (Withdrawn; Currently Amended) A method for the rapid and differential detection of the human endogenous retroviral sequence of the *env* or env and *gag* type, comprising:

(a) making a diagnostic reagent comprising mixing the polynucleotide according to ~~Claim 38~~ Claim 57 with a suitable medium,

(b) preparing a biological tissue or fluid,

(c) extracting a nucleic acid to be detected,

(d) contacting the nucleic acid with said diagnostic reagent,

(e) ~~conducting at least one gene amplification cycle with the aid of said at least one diagnostic reagent,~~

~~(f)~~ detecting a product resulting from a nucleotide sequence-diagnostic reagent interaction, and

~~(g)~~ (f) comparing the nucleic sequences obtained from said detecting with a polynucleotide comprising a sequence containing a polynucleotide fragment that is at least 80% homologous to at least 190 consecutive nucleotides of SEQ ID NO: 1 or at least 90% homologous to at least 700 consecutive nucleotides of SEQ ID NO: 2, wherein said sequence is selected from the group consisting of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, a sequence complementary to one of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22, and a sequence that is the reverse complement to one of SEQ ID NO: ~~3-22, 28 and 61~~ 1, 2, 3-8, 10, 13, 16, 17, and 22.

54. (Withdrawn) The method according to Claim 53, wherein said comparing is by a technique selected from the group consisting of sequencing, Southern blotting, restriction cleavage, and SSCP.

55. (Withdrawn; Currently Amended) A method of making a detection kit, comprising mixing one or more polynucleotides according to ~~Claim 38~~ Claim 57 with at least one reagent selected from the group consisting of the transcripts and cDNAs of the genomic sequences, which encode all or part of a factor, whose function, regulation/de regulation or alteration is associated with the normal or pathological expression or with the regulation/deregulation of motifs belonging to said HERV-7q family, these sequences corresponding to nucleotide sequences encoding genes situated in flanking regions situated upstream and/or downstream of a retroviral sequence of said HERV-7q family, of which one of the ends cannot be at a distance exceeding 120 kb.

56. (Withdrawn) The method according to Claim 55, further comprising attaching said polynucleotide and said reagents to a support.

57. (New) A purified polynucleotide consisting of a polynucleotide sequence selected from the group consisting of:

a) a sequence selected from the group consisting of SEQ ID NO: 3-8, 10, 13, 16, 17, 20, 21, and 22;

b) a complementary sequence to the sequence of a);

c) a reverse complementary sequence to the sequence of a) or b);

d) a fragment derived from the coding region of the sequence of a), wherein said fragment corresponds to a coding frame of at least 14 nucleotides; and

e) a complementary sequence to the sequence of d).

58. (New) The purified polynucleotide according to Claim 57, wherein said fragment in d) consists of SEQ ID NO: 1 or SEQ ID NO: 2.

59. (New) The purified polynucleotide according to Claim 57, wherein said fragment in d) consists of a sequence encoding the C-terminal portion of enverin from amino acid 291

from the first methionine, said sequence starting from the codon at positions 8749 to 8751 of SEQ ID NO: 3.

60. (New) The purified polynucleotide according to Claim 57, wherein said fragment in d) consists of a sequence encoding the C-terminal portion of enverin from amino acid 321 from the first methionine, said sequence starting from the codon at positions 8839 to 8841 of SEQ ID NO: 3.

BASIS FOR THE AMENDMENT

Claims 1-37 were previously canceled.

Claims 38, 39, 44, and 45 have been canceled.

Claims 40, 41, 46, 47, 49, 50, 51, 52, 53, and 55 have been amended.

Claims 57-60 have been added.

The amendment of Claims 40, 41, 46, 47, 49, 50, 51, 52, 53, and 55 and new Claims 57-60 are supported by the claims as originally filed and the specification at pages 1-57.

No new matter is believed to have been added by the present amendment.